

BATCH

RAW SEQUENCE LISTING

DATE: 03/19/2001

PATENT APPLICATION: US/09/680,121A

TIME: 10:16:17

Input Set : A:\Mueth41.app

Output Set: N:\CRF3\03192001\I680121A.raw

3 <110> APPLICANT: French, Cynthia K.
 4 Schneider, Patrick A.
 5 Yamamoto, Karen K.
 7 <120> TITLE OF INVENTION: Prostate Cancer-Specific Marker
 9 <130> FILE REFERENCE: 107-206US-C
 11 <140> CURRENT APPLICATION NUMBER: 09/680,121A
 12 <141> CURRENT FILING DATE: 2000-10-04
 14 <150> PRIOR APPLICATION NUMBER: 60/041,246
 15 <151> PRIOR FILING DATE: 1997-03-07
 17 <150> PRIOR APPLICATION NUMBER: 60/047,811
 18 <151> PRIOR FILING DATE: 1997-05-15
 20 <150> PRIOR APPLICATION NUMBER: 09/036,315
 21 <151> PRIOR FILING DATE: 1998-03-06
 23 <150> PRIOR APPLICATION NUMBER: 09/535,597
 24 <151> PRIOR FILING DATE: 2000-03-27
 26 <160> NUMBER OF SEQ ID NOS: 27
 28 <170> SOFTWARE: PatentIn Ver. 2.1
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 3891
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
 35 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (151)..(1425)
 39 <220> FEATURE:
 40 <223> OTHER INFORMATION: product = Repro-PC-1.0
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 45 cgttccgaaa gccggcgtt gagatccagg caagtgaatc cagccaggca gttttccctt 120
 47 cagcacctcg gacagaacac gcagtaaaaa atg gct ccg atc acc acc agc cgg 174
 48 Met Ala Pro Ile Thr Thr Ser Arg
 49 1 5
 51 gaa gaa ttt gat gaa atc ccc aca gtg gtg ggg atc ttc agt gca ttt 222
 52 Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe
 53 10 15 20
 55 ggc ctg gtc ttc aca gtc tct ctg ttt gca tgg atc tgc tgt cag aga 270
 56 Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg
 57 25 30 35 40
 59 aaa tca tcc aag tct aac aag act cct cca tac aag ttt gtg cat gtg 318
 60 Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val
 61 45 50 55
 63 ctt aag gga gtt gat att tac cct gaa aac cta aat agc aaa aag aag 366
 64 Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys
 65 60 65 70
 67 ttt gga gca gat gat aaa aat gaa gta aag aat aag cca gct gtg cca 414
 68 Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro
 69 75 80 85

ENTERED

See p.5

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71 aag aat tca ttg cat ctg gat ctt gaa aag aga gat ctc aat ggc aat 462
72 Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn
73 90 95 100
75 ttt ccc aaa acc aac ctc aaa cct ggc agt cct tct gat ctg gag aat 510
76 Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn
77 105 110 115 120
79 gca acc ccg aag ctc ttt tta gaa ggg gaa aaa gag tca gtt tcc cct 558
80 Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro
81 125 130 135
83 gag agt tta aag tcc agc act tcc ctt act tca gaa gag aaa caa gag 606
84 Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu
85 140 145 150
87 aag ctg gga act ctc ttc ttc tcc tta gaa tac aac ttc gag aga aaa 654
88 Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys
89 155 160 165
91 gca ttt gtg gtc aat atc aag gaa gcc cgt ggc ttg cca gcc atg gat 702
92 Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro Ala Met Asp
93 170 175 180
95 gag cag tcg atg acc tct gac cca tat atc aaa atg acg atc ctc cca 750
96 Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro
97 185 190 195 200
99 gag aag aag cat aaa gtg aaa act aga gtg ctg aga aaa acc ttg gat 798
100 Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp
101 205 210 215
103 cca gct ttt gat gag acc ttt aca ttc tat ggg ata ccc tac acc caa 846
104 Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln
105 220 225 230
107 atc caa gaa ttg gcc ttg cac ttc aca att ttg agt ttt gac agg ttt 894
108 Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe
109 235 240 245
111 tca aga gat gat atc att ggg gaa gtt cta att cct ctc tcg gga att 942
112 Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile
113 250 255 260
115 gaa tta tct gaa gga aaa atg tta atg aat aga gag atc atc aag aga 990
116 Glu Leu Ser Glu Gly Lys Met Leu Met Asn Arg Glu Ile Ile Lys Arg
117 265 270 275 280
119 aat gtt agg aag tct tca gga cgg ggt gag tta ctg atc tct ctc tgc 1038
120 Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys
121 285 290 295
123 tat cag tcc acc aca aac act cta act gtg gtt gtc tta aaa gct cga 1086
124 Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg
125 300 305 310
127 cat ctg cct aaa tct gat gtg tcc gga ctt tca gat ccc tat gtc aaa 1134
128 His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys
129 315 320 325
131 gtg aac ctg tac cat gcc aaa aag aga atc tcc aag aag aag act cat 1182
132 Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Lys Thr His
133 330 335 340
135 gtg aag aaa tgc acc ccc aat gca gtg ttc aat gag ctg ttt gtc ttt 1230

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136 Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe
137 345 350 355 360
139 gat att cct tgt gag ggc ctt gaa gat ata agt qtt gaa ttt ttg gtt 1278
140 Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser Val Glu Phe Leu Val
141 365 370 375
143 ttg gat tct gaa agg ggg tcc cga aat gag gta atc ggg cag tta gtc 1326
144 Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu Val
145 380 385 390
147 ttg ggt gca gca gaa gga act ggt gga gag cac tgg aaa gag atc 1374
148 Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile
149 395 400 405
151 tgt gac tac ccc agg aga caa att gcc aag tgg cac gtg etc tgt gat 1422
152 Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp
153 410 415 420
155 ggt tagcacccta gccgtgagtt ggaaccttaaa gggttttact aggcaggag 1475
156 Gly
157 425
159 aaattttctt tctttctata ttggattgca agcttgggaa atcaagctac ctttttgttg 1535
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163 ttatgataat ttccctattt attagaagag ttggataaat ttccataaga tattcaatat 1655
165 ctccctcaga ttaccagtga tataactagg aatagtcaga ctttttatga atactgtgcc 1715
167 agaatcccaa attataaatt tgacaatctc attggaacat gtcacaaaaa gttaatgtga 1775
169 ttaagattta aaaacgaaaa gtatgccttg ccttgtgaaa atttatccat ttatcttcag 1835
171 gttgggggaa atcaattttt cttaaatcca aagatactaa aaaaatgtcc tccagtttgt 1895
173 atttattaat tctgtcatgt gcaaatggtt gtccctgcata taaaagtatc tggtcatttc 1955
175 agtttgtgtt gtaattattt gatgcaattt tatcataaga gtaactcaga ttcatttcaa 2015
177 aaggacagtg aacaagctga gaaattattt tatcaaaagg ctgagttgag aacactgtgg 2075
179 ctgaaatata attttctccc cccctaaggt tacatgtgag tcaaaatttt gtaaaatata 2135
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209 taaagaaaaa gtattacatt ctgtatgtac aaagattaaa aatcaacctc ttttttgtgc 3035
211 ttttaaatga cttttggatt aaaaaagcat atttcccaat cattgtcttc attccactac 3095
213 aaagtcacct cacagcatct tgctccactc ggcattctct tgaaagcaac atgaaatgaa 3155
215 ctgtagttag tgtgtagttt ggggaagtca aatggccatt ttatgtatgt gcatttggta 3215
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219 aagtattctt caccgcagcc agaagttaat ggtggtagca gctgaggtat ggttgttgga 3335
221 cgaggccgat tttttttttt taacatggaa caatgaaacc aacaacaaac attttttaaa 3395

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223 ttaaaatgga taatttgtaa atagttttta gcttttataaa tttaaagtgt ttttgagtgt 3455
225 gaaaagtgtga gtaaaactat ttgcaactgg ttttcagaaa agagaaaaga aacacaaaag 3515
227 gaattgaaac aggcagggag atcttaatac ctaatttcat catttctgca aaatgtactg 3575
229 ttttagaatg tattacaata tcaatgtgaa tatcttgaat cctgttacia atcctgcact 3635
231 gtattaaaca tgtaaatata ttgtttgtct gattagccaa tctcaccacc caaatgggga 3695
233 ggtatacatg tttgaagaac gtgtaactcg gtaattgatt tggtctgatg ttgtaactca 3755
235 atagaagtgt tttggaagga agcatggtgt gtgagacagt gtctgttctt ttgtgccagc 3815
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239 aaaaaaaaaa aaaaaa 3891
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245 <213> ORGANISM: Homo sapiens
246 <223> OTHER INFORMATION: product = Repro-PC-1.0
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255 Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
256 35 40 45
258 Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
259 50 55 60
261 Glu Asn Leu Asn Ser Lys Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu
262 65 70 75 80
264 Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu
265 85 90 95
267 Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
268 100 105 110
270 Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu
271 115 120 125
273 Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
274 130 135 140
276 Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser
277 145 150 155 160
279 Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu
280 165 170 175
282 Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
283 180 185 190
285 Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
286 195 200 205
288 Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr
289 210 215 220
291 Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe
292 225 230 235 240
294 Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu
295 245 250 255
297 Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu
298 260 265 270

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/680,121A

541: 937: 1770-11

531 : 76 : 19 : 17

Input Set : A:\Mueth41.app

Output Set: N:\CRF3\03192001\I580121A.raw

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303      290      295      300
304 Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser
305      305      310      315
306 Glu Leu Ser Asp Pro Thr Val Lys Val Asn Leu Leu His Ala Lys Lys
307      315      320      325
308 Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala
309      330      335      340
310 Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu
311      345      350      355
312 Asp Ile Ser Val Thr Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
313      360      365      370
314 Asn Glu Val Ile Gly Glu Leu Val Leu Gly Ala Ala Ala Glu Gly Thr
315      375      380      385
316 Gly Gly Glu His Trp Lys Glu Ile Cys Asp Tyr Pro Arg Arg Glu Ile
317      390      395      400
318 Ala Lys Trp His Val Leu Cys Asp Gly
319      405      410      415
320      420      425
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322 <211> LENGTH: 21
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324 <213> ORGANISM: Homo sapiens
325 <220> FEATURE:
326 <221> NAME/KEY: misc_feature
327 <222> LOCATION: (1)..(21)
328 <223> OTHER INFORMATION: 5' oligo (109) Upper Primer
329 <400> SEQUENCE: 3
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331      21
332 <210> SEQ ID NO: 4
333 <211> LENGTH: 30
334 <212> TYPE: DNA
335 <213> ORGANISM: Homo sapiens
336 <220> FEATURE:
337 <221> NAME/KEY: misc_feature
338 <222> LOCATION: (1)..(30)
339 <223> OTHER INFORMATION: 3' oligo (3489) Lower Primer
340 <400> SEQUENCE: 4
341 tttcttcttctt ctttcttctt tcttcttctt
342      30
343 <210> SEQ ID NO: 5
344 <211> LENGTH: 125
345 <212> TYPE: PRF
346 <213> ORGANISM: rat
347 <220> FEATURE:
348 <223> OTHER INFORMATION: residues 1-125 = rat synaptotagmin 4 (SYT4)
349 <400> SEQUENCE: 5
350 Met Ala Pro Ile Thr Thr Ser Arg Val Glu Phe Asp Glu Ile Pro Thr
351      1      5      10      15

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Please Note:

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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TIME: 10:16:18

Input Set : A:\Mueth41.app

Output Set: N:\CRF3\03192001\I680121A.raw

L:651 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:651 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:651 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:670 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:670 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:670 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:686 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:686 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:686 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
L:702 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:702 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
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L:722 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:742 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:742 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:742 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:758 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:758 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
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L:774 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:774 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
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L:809 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
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L:809 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:915 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:915 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:915 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27